Kar-Chun Tan

List of Publications by Year in descending order

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ΚΛΡ-CHIIN ΤΛΝ

#	Article	IF	CITATIONS
1	Dothideomycete–Plant Interactions Illuminated by Genome Sequencing and EST Analysis of the Wheat Pathogen <i>Stagonospora nodorum</i> . Plant Cell, 2007, 19, 3347-3368.	6.6	235
2	The nutrient supply of pathogenic fungi; a fertile field for study. Molecular Plant Pathology, 2003, 4, 203-210.	4.2	195
3	SnTox3 Acts in Effector Triggered Susceptibility to Induce Disease on Wheat Carrying the Snn3 Gene. PLoS Pathogens, 2009, 5, e1000581.	4.7	175
4	Stagonospora nodorum: cause of stagonospora nodorum blotch of wheat. Molecular Plant Pathology, 2006, 7, 147-156.	4.2	153
5	Assessing the impact of transcriptomics, proteomics and metabolomics on fungal phytopathology. Molecular Plant Pathology, 2009, 10, 703-715.	4.2	121
6	Accessories Make the Outfit: Accessory Chromosomes and Other Dispensable DNA Regions in Plant-Pathogenic Fungi. Molecular Plant-Microbe Interactions, 2018, 31, 779-788.	2.6	93
7	The Disruption of a Gα Subunit Sheds New Light on the Pathogenicity of Stagonospora nodorum on Wheat. Molecular Plant-Microbe Interactions, 2004, 17, 456-466.	2.6	83
8	Proteinaceous necrotrophic effectors in fungal virulence. Functional Plant Biology, 2010, 37, 907.	2.1	80
9	Differential effector gene expression underpins epistasis in a plant fungal disease. Plant Journal, 2016, 87, 343-354.	5.7	75
10	Regulation of proteinaceous effector expression in phytopathogenic fungi. PLoS Pathogens, 2017, 13, e1006241.	4.7	75
11	Quantitative Variation in Effector Activity of ToxA Isoforms from <i>Stagonospora nodorum</i> and <i>Pyrenophora tritici-repentis</i> . Molecular Plant-Microbe Interactions, 2012, 25, 515-522.	2.6	70
12	A functionally conserved Zn ₂ Cys ₆ binuclear cluster transcription factor class regulates necrotrophic effector gene expression and hostâ€specific virulence of two major Pleosporales fungal pathogens of wheat. Molecular Plant Pathology, 2017, 18, 420-434.	4.2	69
13	The Transcription Factor StuA Regulates Central Carbon Metabolism, Mycotoxin Production, and Effector Gene Expression in the Wheat Pathogen Stagonospora nodorum. Eukaryotic Cell, 2010, 9, 1100-1108.	3.4	63
14	Mannitol 1-Phosphate Metabolism Is Required for Sporulation in Planta of the Wheat Pathogen Stagonospora nodorum. Molecular Plant-Microbe Interactions, 2005, 18, 110-115.	2.6	53
15	Novel sources of resistance to Septoria nodorum blotch in the Vavilov wheat collection identified by genome-wide association studies. Theoretical and Applied Genetics, 2018, 131, 1223-1238.	3.6	53
16	A quantitative PCR approach to determine gene copy number. Fungal Genetics Reports, 2008, 55, 5-8.	0.6	53
17	Transcription factor control of virulence in phytopathogenic fungi. Molecular Plant Pathology, 2021, 22, 858-881.	4.2	50
18	Metabolite profiling identifies the mycotoxin alternariol in the pathogen Stagonospora nodorum. Metabolomics, 2009, 5, 330-335.	3.0	48

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19	Assessing European Wheat Sensitivities to Parastagonospora nodorum Necrotrophic Effectors and Fine-Mapping the Snn3-B1 Locus Conferring Sensitivity to the Effector SnTox3. Frontiers in Plant Science, 2018, 9, 881.	3.6	48
20	Genetic mapping using a wheat multi-founder population reveals a locus on chromosome 2A controlling resistance to both leaf and glume blotch caused by the necrotrophic fungal pathogen Parastagonospora nodorum. Theoretical and Applied Genetics, 2020, 133, 785-808.	3.6	48
21	Comprehensive Annotation of the Parastagonospora nodorum Reference Genome Using Next-Generation Genomics, Transcriptomics and Proteogenomics. PLoS ONE, 2016, 11, e0147221.	2.5	47
22	A Signaling-Regulated, Short-Chain Dehydrogenase of <i>Stagonospora nodorum</i> Regulates Asexual Development. Eukaryotic Cell, 2008, 7, 1916-1929.	3.4	45
23	Pan-Parastagonospora Comparative Genome Analysis—Effector Prediction and Genome Evolution. Genome Biology and Evolution, 2018, 10, 2443-2457.	2.5	43
24	Fine-Mapping the Wheat <i>Snn1</i> Locus Conferring Sensitivity to the <i>Parastagonospora nodorum</i> Necrotrophic Effector SnTox1 Using an Eight Founder Multiparent Advanced Generation Inter-Cross Population. G3: Genes, Genomes, Genetics, 2015, 5, 2257-2266.	1.8	38
25	Sensitivity to three Parastagonospora nodorum necrotrophic effectors in current Australian wheat cultivars and the presence of further fungal effectors. Crop and Pasture Science, 2014, 65, 150.	1.5	37
26	Spatial and temporal coordination of expression of immune response genes during Pseudomonas infection of horseshoe crab, Carcinoscorpius rotundicauda. Genes and Immunity, 2005, 6, 557-574.	4.1	34
27	A specific fungal transcription factor controls effector gene expression and orchestrates the establishment of the necrotrophic pathogen lifestyle on wheat. Scientific Reports, 2019, 9, 15884.	3.3	34
28	Deep proteogenomics; high throughput gene validation by multidimensional liquid chromatography and mass spectrometry of proteins from the fungal wheat pathogen Stagonospora nodorum. BMC Bioinformatics, 2009, 10, 301.	2.6	33
29	Functional redundancy of necrotrophic effectors – consequences for exploitation for breeding. Frontiers in Plant Science, 2015, 6, 501.	3.6	33
30	Analysis of Reproducibility of Proteome Coverage and Quantitation Using Isobaric Mass Tags (iTRAQ) Tj ETQq0 C	0 ggBT /O	verlock 10 T
31	Quantitative proteomic analysis of Gâ€protein signalling in <i>Stagonospora nodorum</i> using isobaric tags for relative and absolute quantification. Proteomics, 2010, 10, 38-47.	2.2	25
32	Proteomic identification of extracellular proteins regulated by the Gna1 G $\hat{I}\pm$ subunit in Stagonospora nodorum. Mycological Research, 2009, 113, 523-531.	2.5	24
33	Septoria Nodorum Blotch of Wheat: Disease Management and Resistance Breeding in the Face of Shifting Disease Dynamics and a Changing Environment. Phytopathology, 2021, 111, 906-920.	2.2	24
34	Genomeâ€Wide Association Mapping of Resistance to Septoria Nodorum Leaf Blotch in a Nordic Spring Wheat Collection. Plant Genome, 2019, 12, 180105.	2.8	22
35	Absence of detectable yield penalty associated with insensitivity to <scp>P</scp> leosporales necrotrophic effectors in wheat grown in the <scp>W</scp> est <scp>A</scp> ustralian wheat belt. Plant Pathology, 2014, 63, 1027-1032.	2.4	20
36	Development of genetic <scp>SSR</scp> markers in <i>Blumeria graminis</i> f. sp. <i>hordei</i> and application to isolates from Australia. Plant Pathology, 2015, 64, 337-343.	2.4	16

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37	Low Amplitude Boom-and-Bust Cycles Define the Septoria Nodorum Blotch Interaction. Frontiers in Plant Science, 2019, 10, 1785.	3.6	16
38	Vavilov wheat accessions provide useful sources of resistance to tan spot (syn. yellow spot) of wheat. Plant Pathology, 2018, 67, 1076-1087.	2.4	15
39	Chromosome-level genome assembly and manually-curated proteome of model necrotroph Parastagonospora nodorum Sn15 reveals a genome-wide trove of candidate effector homologs, and redundancy of virulence-related functions within an accessory chromosome. BMC Genomics, 2021, 22, 382.	2.8	12
40	Necrotrophic Pathogens of Wheat. , 2016, , 273-278.		11
41	Identification and cross-validation of genetic loci conferring resistance to Septoria nodorum blotch using a German multi-founder winter wheat population. Theoretical and Applied Genetics, 2021, 134, 125-142.	3.6	11
42	Hidden in plain sight: a molecular field survey of three wheat leaf blotch fungal diseases in North-Western Europe shows co-infection is widespread. European Journal of Plant Pathology, 2021, 160, 949-962.	1.7	9
43	Dissecting the role of histidine kinase and HOG1 mitogen-activated protein kinase signalling in stress tolerance and pathogenicity of Parastagonospora nodorum on wheat. Microbiology (United) Tj ETQq1 1 0.784	1314 rg8T /(Oveølock 10 T
44	Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat. PLoS Pathogens, 2022, 18, e1010149.	4.7	9
45	GWAS analysis reveals distinct pathogenicity profiles of Australian Parastagonospora nodorum isolates and identification of marker-trait-associations to septoria nodorum blotch. Scientific Reports, 2021, 11, 10085.	3.3	7
46	Proteomic Techniques for Plant–Fungal Interactions. Methods in Molecular Biology, 2012, 835, 75-96.	0.9	4
47	Transcription factor lineages in plant-pathogenic fungi, connecting diversity with fungal virulence. Fungal Genetics and Biology, 2022, 161, 103712.	2.1	4
48	Gene Validation and Remodelling Using Proteogenomics of Phytophthora cinnamomi, the Causal Agent of Dieback. Frontiers in Microbiology, 2021, 12, 665396.	3.5	3
49	An optimized sporulation method for the wheat fungal pathogen Pyrenophora tritici-repentis. Plant Methods, 2021, 17, 52.	4.3	2
50	12 Metabolomics and Proteomics to Dissect Fungal Phytopathogenicity. , 2014, , 301-319.		1